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$$AV = \frac{1}{2} \left( \frac{V_{\text{max}}}{V_{\text{min}}} + \frac{V_{\text{min}}}{V_{\text{max}}} \right) \quad (1)$$

$$\Delta V = \frac{1}{2} \left( \frac{V_{\text{max}}}{V_{\text{min}}} - \frac{V_{\text{min}}}{V_{\text{max}}} \right) \quad (2)$$

where  $V_{\text{max}}$  and  $V_{\text{min}}$  are the maximum and minimum values of the voltage, respectively. The average voltage (AV) and the voltage difference ( $\Delta V$ ) are calculated from the following equations:

$$AV = \frac{1}{2} \left( \frac{V_{\text{max}}}{V_{\text{min}}} + \frac{V_{\text{min}}}{V_{\text{max}}} \right) \quad (1)$$

$$\Delta V = \frac{1}{2} \left( \frac{V_{\text{max}}}{V_{\text{min}}} - \frac{V_{\text{min}}}{V_{\text{max}}} \right) \quad (2)$$



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The figure consists of seven small, square micrographs arranged in a vertical column, each showing a different stage of embryonic development. The stages are numbered 1 through 7 from top to bottom. Stage 1 shows a single cell with a prominent nucleus. Stage 2 shows two cells. Stage 3 shows four cells in a 2x2 arrangement. Stage 4 shows eight cells in a more complex pattern. Stage 5 shows a hollow sphere of cells (blastula). Stage 6 shows a more developed blastula with internal structures visible. Stage 7 shows a hatched embryo, which is a small, elongated organism with a distinct head and tail.

[illegible]

1. **Identify the main idea of the passage.**  
 2. **Summarize the main idea in your own words.**  
 3. **Identify the supporting details.**  
 4. **Summarize the supporting details in your own words.**  
 5. **Identify the conclusion.**  
 6. **Summarize the conclusion in your own words.**  
 7. **Identify the author's purpose.**  
 8. **Summarize the author's purpose in your own words.**  
 9. **Identify the author's tone.**  
 10. **Summarize the author's tone in your own words.**  
 11. **Identify the author's style.**  
 12. **Summarize the author's style in your own words.**  
 13. **Identify the author's audience.**  
 14. **Summarize the author's audience in your own words.**  
 15. **Identify the author's message.**  
 16. **Summarize the author's message in your own words.**  
 17. **Identify the author's theme.**  
 18. **Summarize the author's theme in your own words.**  
 19. **Identify the author's genre.**  
 20. **Summarize the author's genre in your own words.**

[illegible][illegible][illegible]

Figure 1: Schematic representation of the experimental design. The diagram shows a sequence of events: 'Stimulus presentation' (a box with a question mark), 'Response' (a box with a question mark), 'Feedback' (a box with a question mark), and 'Inter-trial interval' (a box with a question mark). The sequence is repeated for multiple trials, with a 'Start' box at the beginning and an 'End' box at the end.

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DB 183 GESLSRKE 190

RESULT 11

AAK38793

1D AAK38793 standard; protein: 216 AA.

XX AAK38793:

DI 21-JAN-1994 (first entry)

DE Natural human interferon alpha.

KW IFN-alpha; hIFN-alpha.

OS Homo sapiens.

XX Key Location/qualifiers

FT Region /note= "Natural mature human alpha-interferon N-terminal"

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FT Region /note= "Natural mature human alpha-interferon N-terminal"

FT Region /note= "Natural mature human alpha-interferon N-terminal"

FT Region /note= "Natural mature human alpha-interferon N-terminal"

EP55494-A.

04 A06-1993.

29-DEC-1992: 92EP-0122084.

31-DEC-1991: 91KR-0025678.

31-DEC-1991: 91KR-0025679.

28-JAN-1992: 92KR-0001195.

(LOCK-) LOCKY LTB.

Hao TQ, Chang HJ, Cho JM, Park SO, Park W.

WPI: 1993-244546/31.

N-PSDR: AA047151.

Recombinant human alpha interferon and corresponding

efficient expression in yeast and purification process

Disclosures: Fig 1b; 30pp; English.

The sequence is that of natural human interferon-alpha.

Sequence 216 AA:

Query Match 99.78; Score 957; DB 14; Length 216

Best Local Similarity 99.58; Prod. No. 3, 6e-09;

Matches 187; Conservative 1; Mismatches 9; Indels 0; Gap 0

1 MATFATVAVTIVSRSSSVSTTPATSESTSEPTIMAVPESTVSTKTHQV

3 MATFATVAVTIVSRSSSVSTTPATSESTSEPTIMAVPESTVSTKTHQV

61 FVQEPFQNOFQKALIVLHMVQVINCSTFSSVAVGTFILKQVTHVAVLQV

63 FVQEPFQNOFQKALIVLHMVQVINCSTFSSVAVGTFILKQVTHVAVLQV

123 CVIGVWVTPVPRFSTVAVPESTVSTKTHQVINCSTFSSVAVGTFILKQVTHVAVLQV

123 CVIGVWVTPVPRFSTVAVPESTVSTKTHQVINCSTFSSVAVGTFILKQVTHVAVLQV

181 GESLSRKE 188

183 GESLSRKE 190

RESULT 12

AAK38793

1D AAK38793 standard; protein: 183 AA.

XX AAK38793:

DI 21-JAN-1994 (first entry)

DE Natural human interferon alpha.

KW IFN-alpha; hIFN-alpha.

OS Homo sapiens.

XX Key Location/qualifiers

FT Region /note= "Natural mature human alpha-interferon N-terminal"

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EP55494-A.

04 A06-1993.

29-DEC-1992: 92EP-0122084.

31-DEC-1991: 91KR-0025678.

31-DEC-1991: 91KR-0025679.

28-JAN-1992: 92KR-0001195.

(LOCK-) LOCKY LTB.

Hao TQ, Chang HJ, Cho JM, Park SO, Park W.

WPI: 1993-244546/31.

N-PSDR: AA047151.

Recombinant human alpha interferon and corresponding

efficient expression in yeast and purification process

Disclosures: Fig 1b; 30pp; English.

The sequence is that of natural human interferon-alpha.

Sequence 183 AA:

Query Match 99.78; Score 957; DB 14; Length 216

Best Local Similarity 99.58; Prod. No. 3, 6e-09;

Matches 187; Conservative 1; Mismatches 9; Indels 0; Gap 0

1 MATFATVAVTIVSRSSSVSTTPATSESTSEPTIMAVPESTVSTKTHQV

3 MATFATVAVTIVSRSSSVSTTPATSESTSEPTIMAVPESTVSTKTHQV

61 FVQEPFQNOFQKALIVLHMVQVINCSTFSSVAVGTFILKQVTHVAVLQV

63 FVQEPFQNOFQKALIVLHMVQVINCSTFSSVAVGTFILKQVTHVAVLQV

123 CVIGVWVTPVPRFSTVAVPESTVSTKTHQVINCSTFSSVAVGTFILKQVTHVAVLQV

123 CVIGVWVTPVPRFSTVAVPESTVSTKTHQVINCSTFSSVAVGTFILKQVTHVAVLQV

181 GESLSRKE 188

183 GESLSRKE 190



DB 121 VVGGVWVTHIMKTS...  
QY 181 QESLSRKE 188  
DB 181 QESLSRKE 188

RESULT 15

AAP20007  
ID AAP20007 standard: protein: 187 AA.

AC AAP20007:

UT 18-DEC-1992 (first entry)

DE Hybrid human leukocyte interferon LeIFN.

XX Leukocyte; interferon; antitumor; immunostimulant; viraride; protein;  
KW pl-c1FA.

XX Homo sapiens.

XX EP51873-A.

XX 19 MAY-1982.

XX 09-NOV-1981; 8108-0109579.

XX 25-SEP-1981; 8108-0405579.

XX 10-NOV-1980; 8008-0205579.

XX 23-FEB-1981; 8108-0247884.

XX (GENE-) GENENTECH INC.

XX (Goodel) DYN.

XX WPI: 1982-417884/21 (417884).

XX N-PSDB; AAN20005.

XX Hybrid human leukocyte interferon(s) - useful for treatment of  
PI and neoplastic diseases

XX Disclosure; fig 1; 54pp; English.

XX This protein is expressed in Escherichia coli using the replication  
CC expression vector plasmid pUC-119. See also AAN20005, AAN20026, AAN20027  
CC and AAP20008-14.

XX Sequence 187 AA;

Query Match 98.4%; Score 944; DB 4; (004) 107;

Best Local Similarity 96.4%; Prod. No. 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100;

DB 1 ALFAIIVAVIVISKSSSVQV...  
QY 52 FGEFGRDPOKAEITV...  
DB 61 FGEFGRDPOKAEITV...

QY 121 VVGGVWVTHIMKTS...  
DB 121 VVGGVWVTHIMKTS...

QY 181 QESLSRKE 188  
DB 181 QESLSRKE 188

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Search completed: January 17, 2003, 06:53:54  
Job time : 59.1926 secs







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exon	3477	3538		+	8	/number=6 /gene="Adhl-1s"
intron	3539	3625		+	9	/number=7 /gene="Adhl-1s"
exon	3626	3721		+	10	/number=7 /gene="Adhl-1s"
intron	3722	3812		+	11	/number=8 /gene="Adhl-1s"
exon	3813	3974		+	12	/number=8 /gene="Adhl-1s"
intron	3975	4064		+	13	/number=9 /gene="Adhl-1s"
exon	4065	4181		+	14	/number=9 /gene="Adhl-1s"
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polyA_site	4405	4415		+	17	
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repeat_region	4449	4452		+	19	
repeat_region	4453	4456		+	20	
repeat_region	4457	4460		+	21	
repeat_region	4461	4464		+	22	
repeat_region	4465	4468		+	23	
repeat_region	4469	4472		+	24	
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repeat_region						

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Figure 1. The effect of the *in vitro* incubation time on the release of *in vivo* released  $^{125}$ I-labelled  $\alpha$ - $\beta$  casein from the *in vitro* incubated microsomes. The microsomes were incubated for 10 min, 30 min, 1 h, 2 h, 4 h, 8 h, 16 h, 32 h, 64 h, 128 h, 256 h, 512 h, 1024 h, 2048 h, 4096 h, 8192 h, 16384 h, 32768 h, 65536 h, 131072 h, 262144 h, 524288 h, 1048576 h, 2097152 h, 4194304 h, 8388608 h, 16777216 h, 33554432 h, 67108864 h, 134217728 h, 268435456 h, 536870912 h, 1073741824 h, 2147483648 h, 4294967296 h, 8589934592 h, 17179869184 h, 34359738368 h, 68719476736 h, 137438953472 h, 274877906944 h, 549755813888 h, 1099511627776 h, 2199023255552 h, 4398046511104 h, 8796093022208 h, 17592186044416 h, 35184372088832 h, 70368744177664 h, 140737488355328 h, 281474976710656 h, 562949953421312 h, 1125899906842624 h, 2251799813685248 h, 4503599627370496 h, 9007199254740992 h, 18014398509481984 h, 36028797018963968 h, 72057594037927936 h, 144115188075855872 h, 288230376151711744 h, 576460752303423488 h, 1152921504606846976 h, 2305843009213693952 h, 4611686018427387904 h, 9223372036854775808 h, 18446744073709551616 h, 36893488147419103232 h, 73786976294838206464 h, 147573952589676412928 h, 295147905179352825856 h, 590295810358705651712 h, 1180591620717411303424 h, 2361183241434822606848 h, 4722366482869645213696 h, 9444732965739290427392 h, 18889465931478580854784 h, 37778931862957161709568 h, 75557863725914323419136 h, 151115727451828646838272 h, 302231454903657293676544 h, 604462909807314587353088 h, 1208925819614629174706176 h, 2417851639229258349412352 h, 4835703278458516698824704 h, 9671406556917033397649408 h, 19342813113834066795298816 h, 38685626227668133590597632 h, 77371252455336267181195264 h, 154742504910672534362390528 h, 309485009821345068724781056 h, 618970019642690137449562112 h, 1237940039285380274899124224 h, 2475880078570760549798248448 h, 4951760157141521099596496896 h, 9903520314283042199192993792 h, 19807040628566084398385987584 h, 39614081257132168796771975168 h, 79228162514264337593543950336 h, 158456325028528675187087900672 h, 316912650057057350374175801344 h, 633825300114114700748351602688 h, 1267650600228229401496703205376 h, 2535301200456458802993406410752 h, 5070602400912917605986812821504 h, 10141204801825835211973625643008 h, 20282409603651670423947251286016 h, 40564819207303340847894502572032 h, 81129638414606681695789005144064 h, 162259276829213363391578010288128 h, 324518553658426726783156020576256 h, 649037107316853453566312041152512 h, 1298074214633706907132624082305024 h, 2596148429267413814265248164610048 h, 5192296858534827628530496329220096 h, 10384593717069655257060992658440192 h, 20769187434139310514121985316880384 h, 41538374868278621028243970633760768 h, 83076749736557242056487941267521536 h, 166153499473114484112975882535043072 h, 332306998946228968225951765070086144 h, 664613997892457936451903530140172288 h, 1329227995784915872903807060280344576 h, 2658455991569831745807614120560689152 h, 5316911983139663491615228241121378304 h, 10633823966279326983230456482242756608 h, 21267647932558653966460912964485513216 h, 42535295865117307932921825928971026432 h, 85070591730234615865843651857942052864 h, 170141183460469231731687303715884105728 h, 340282366920938463463374607431768211456 h, 680564733841876926926749214863536422912 h, 1361129467683753853853498429727072845824 h, 2722258935367507707706996859454145691648 h, 5444517870735015415413993718908291383296 h, 10889035741470030830827987437816582766592 h, 21778071482940061661655974875633165533184 h, 43556142965880123323311949751266331066368 h, 87112285931760246646623899502532662132736 h, 174224571863520493293247799005065324265472 h, 348449143727040986586495598010130648530944 h, 696898287454081973172991196020261297061888 h, 1393796574908163946345982392040522594123776 h, 2787593149816327892691964784081045188247552 h, 5575186299632655785383929568162090376495104 h, 11150372599265311570767859136324180752990208 h, 22300745198530623141535718272648361505980416 h, 44601490397061246283071436545296723011960832 h, 89202980794122492566142873090593446023921664 h, 178405961588244985132285746181186892047843328 h, 356811923176489970264571492362373784095686656 h, 713623846352979940529142984724747568191373312 h, 1427247692705959881058285969449495136382746624 h, 2854495385411919762116571938898990272765493248 h, 57089907708238

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3201 3202 3203 3204 3205 3206 3207 3208 3209 3210 3211 3212 3213 3214 3215 3216 3217 3218 3219 3220 3221 3222 3223 3224 3225 3226 3227 3228 3229 3230 3231 3232 3233 3234 3235 3236 3237 3238 3239 3240 3241 3242 3243 3244 3245 3246 3247 3248 3249 3250 3251 3252 3253 3254 3255 3256 3257 3258 3259 3260 3261 3262 3263 3264 3265 3266 3267 3268 3269 3270 3271 3272 3273 3274 3275 3276 3277 3278 3279 3280 3281 3282 3283 3284 3285 3286 3287 3288 3289 3290 3291 3292 3293 3294 3295 3296 3297 3298 3299 3300 3301 3302 3303 3304 3305 3306 3307 3308 3309 3310 3311 3312 3313 3314 3315 3316 3317 3318 3319 3320 3321 3322 3323 3324 3325 3326 3327 3328 3329 3330 3331 3332 3333 3334 3335 3336 3337 3338 3339 3340 3341 3342 3343 3344 3345 3346 3347 3348 3349 3350 3351 3352 3353 3354 3355 3356 3357 3358 3359 3360 3361 3362 3363 3364 3365 3366 3367 3368 3369 3370 3371 3372 3373 3374 3375 3376 3377 3378 3379 3380 3381 3382 3383 3384 3385 3386 3387 3388 3389 3390 3391 3392 3393 3394 3395 3396 3397 3398 3399 3400 3401 3402 3403 3404 3405 3406 3407 3408 3409 3410 3411 3412 3413 3414 3415 3416 3417 3418 3419 3420 3421 3422 3423 3424 3425 3426 3427 3428 3429 3430 3431 3432 3433 3434 3435 3436 3437 3438 3439 3440

















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US-05-915-873-3 (1-96) X US-08-482-920-6 (1-44)

APPLICANT: Dawson, William O.  
APPLICANT: Grantham, George L.  
APPLICANT: Turpen, Thomas H.  
APPLICANT: Turpen, Ann Myers  
APPLICANT: Garper, Stephen J.  
APPLICANT: Gull, Lawrence R.  
TITLE OF INVENTION: RECOMBINANT PLANT VITAMINOLYTIC ACTIVITY  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lemmie & Edmunds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
PRIORITY NUMBER: 82-003-493-620  
FILING DATE: 07-JUNE 1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 184,217  
FILING DATE: 19-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 600,244  
FILING DATE: 22-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 641,617  
FILING DATE: 16-JAN-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 410,881  
FILING DATE: 17-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 160,766  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 160,771  
FILING DATE: 26-FEB-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 347,637  
FILING DATE: 05-MAY-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 365,138  
FILING DATE: 08-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 219,279  
FILING DATE: 15-JUL-1988  
ALTERNATIVE AGENT INFORMATION:  
NAME: Halliwell, Albert P.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET INFORMATION: 8129 112  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3654  
INFORMATION FOR SEQ. ID NO.: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 444 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MULTIPLE TYPE: protein  
US-08-482-920-6

Alignment Scores:  
Pred. No.: 3,218-12  
Score: 144.60  
Percent Similarity: 100.00%  
Host Local Similarity: 100.00%  
Query Match: 82.02%  
OH: 2  
Gaps: 0

Inserts: 44  
Matches: 31  
Conserved: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

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|------------------------|----------|---------------|----|
| Score: No.:            | 3.21e+12 | Length:       | 4  |
| Score:                 | 146, 00  | Matches:      | 41 |
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| Best Local Similarity: | 100.00%  | Mismatch:     | 0  |
| Query Match:           | 82.02%   | Indel:        | 0  |
| DB:                    | 4        | Gaps:         | 0  |































LENGTH: 165  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-740-464-1

Query Match 66.44: 99.44: 99.44: 99.44: 99.44: 99.44:  
Best Local Similarity 99.44: Pred. No. 5, 60-91:  
Matches 164: Conservative 0: Mismatches 1: Indels 0: Gaps 0

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DB 1 CILPHTSNLSPEFLMLAKMRLSSCKKIMHSGFVLRHNPQNAELIVYHMF 60  
QY 61 GQENIPESTRSSAMPTIDKRYTPIYQNLNLELVGVGVVHPIHMFHSLAVK 120  
DB 61 GQENIPESTRSSAMPTIDKRYTPIYQNLNLELVGVGVVHPIHMFHSLAVK 120  
QY 121 RYFPEFLYIKRKYSPVAMVAVHRESESTENASLSEED 120  
DB 121 RYFPEFLYIKRKYSPVAMVAVHRESESTENASLSEED 120  
QY 121 RYFPEFLYIKRKYSPVAMVAVHRESESTENASLSEED 120  
DB 121 RYFPEFLYIKRKYSPVAMVAVHRESESTENASLSEED 120

RESULT 12  
US-08-249-671A-5

Sequence 5, Application 75/0824671A  
Patent No. 5710027

GENERAL INFORMATION:

APPLICANT: Haploplan, K.

APPLICANT: Falkner, E.

APPLICANT: Bodo, G.

APPLICANT: Voa, T.

TITLE OF INVENTION: Process for preparing and purified

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESS: 1100 New York Avenue, Suite 600

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25 (PRT)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/0824671A

FILING DATE: 26-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 42,893

REFERENCE/DOCKET NUMBER: 0052 1350000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 165 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-249-671A-5

Query Match 99.14: Score 844: DB 1: Length 164:

Best Local Similarity 99.44: Pred. No. 9, 60-91:

Matches 164: Conservative 0: Mismatches 1: Indels 0: Gaps 0

QY 1 CILPHTSNLSPEFLMLAKMRLSSCKKIMHSGFVLRHNPQNAELIVYHMF 60  
DB 1 CILPHTSNLSPEFLMLAKMRLSSCKKIMHSGFVLRHNPQNAELIVYHMF 60

QY 1 CILPHTSNLSPEFLMLAKMRLSSCKKIMHSGFVLRHNPQNAELIVYHMF 60  
DB 1 CILPHTSNLSPEFLMLAKMRLSSCKKIMHSGFVLRHNPQNAELIVYHMF 60  
QY 61 GQENIPESTRSSAMPTIDKRYTPIYQNLNLELVGVGVVHPIHMFHSLAVK 120  
DB 61 GQENIPESTRSSAMPTIDKRYTPIYQNLNLELVGVGVVHPIHMFHSLAVK 120  
QY 121 RYFPEFLYIKRKYSPVAMVAVHRESESTENASLSEED 120  
DB 121 RYFPEFLYIKRKYSPVAMVAVHRESESTENASLSEED 120

RESULT 13  
US-08-249-671A-5

Sequence 11, Application 75/0824671A  
Patent No. 5710027

GENERAL INFORMATION:

APPLICANT: Haploplan, K.

APPLICANT: Falkner, E.

APPLICANT: Bodo, G.

APPLICANT: Voa, T.

TITLE OF INVENTION: Process for preparing and purified

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESS: 1100 New York Avenue, Suite 600

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25 (PRT)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 05/0824671A

FILING DATE: 26-MAY-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 42,893

REFERENCE/DOCKET NUMBER: 0052 1350000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 165 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-249-671A-5

Query Match 99.14: Score 844: DB 1: Length 164:

Best Local Similarity 99.44: Pred. No. 9, 60-91:

Matches 164: Conservative 0: Mismatches 1: Indels 0: Gaps 0

QY 1 CILPHTSNLSPEFLMLAKMRLSSCKKIMHSGFVLRHNPQNAELIVYHMF 60  
DB 1 CILPHTSNLSPEFLMLAKMRLSSCKKIMHSGFVLRHNPQNAELIVYHMF 60

QY 61 GQENIPESTRSSAMPTIDKRYTPIYQNLNLELVGVGVVHPIHMFHSLAVK 120  
DB 61 GQENIPESTRSSAMPTIDKRYTPIYQNLNLELVGVGVVHPIHMFHSLAVK 120

QY 121 RYFPEFLYIKRKYSPVAMVAVHRESESTENASLSEED 120  
DB 121 RYFPEFLYIKRKYSPVAMVAVHRESESTENASLSEED 120

QY 121 RYFPEFLYIKRKYSPVAMVAVHRESESTENASLSEED 120  
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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 06:50:48 : Search time 9.000 seconds  
(with 90 alignments)  
692,500 M1150b v11 updates/sw

Title: US-09-915-873-4

Perfect score: 960

Sequence: 1 MALTALLVALLVSKSSR.....SMPKTSSTVLSKMKKE 122

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 28424 seqs, 9511422 positions

Total number of hits satisfying chosen parameters: 28424

Minimum db seq length: 0  
Maximum db seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%

Listing first 45 summaries

Database : PIR\_73:  
1: p1f1:  
2: p1f2:  
3: p1f3:  
4: p1f4:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being returned, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 957   | 99.7        | 188    | 1     | 1VH0A2      |
| 2          | 851   | 88.6        | 165    | 1     | 176570      |
| 3          | 809.5 | 84.3        | 189    | 1     | 1VH0A7      |
| 4          | 808.5 | 84.2        | 189    | 1     | 1VH016      |
| 5          | 793.5 | 82.7        | 189    | 1     | 1VH014      |
| 6          | 781.5 | 81.4        | 189    | 2     | 152347      |
| 7          | 779.5 | 81.2        | 189    | 2     | 151970      |
| 8          | 772.5 | 80.5        | 189    | 1     | 1VH0A1      |
| 9          | 770.5 | 80.3        | 189    | 1     | 1VH0A8      |
| 10         | 768.5 | 80.1        | 189    | 2     | 164464      |
| 11         | 767.5 | 79.9        | 189    | 1     | 1VH015      |
| 12         | 765.5 | 79.8        | 189    | 1     | 1VH016      |
| 13         | 765.5 | 79.8        | 189    | 1     | 1VH0A5      |
| 14         | 760.5 | 79.2        | 189    | 1     | 1VH0A9      |
| 15         | 756.5 | 78.8        | 189    | 2     | 142584      |
| 16         | 754.5 | 78.6        | 189    | 1     | 1VH018      |
| 17         | 748.5 | 78.0        | 189    | 2     | 154102      |
| 18         | 744.5 | 77.6        | 189    | 1     | 1VH0A0      |
| 19         | 740.5 | 77.0        | 181    | 2     | 156413      |
| 20         | 742.5 | 76.4        | 156    | 1     | 1VH0A4      |
| 21         | 738.5 | 75.9        | 176    | 2     | 156114      |
| 22         | 732.5 | 75.3        | 184    | 1     | 1VH0A4      |
| 23         | 719.5 | 74.9        | 167    | 2     | 025843      |
| 24         | 718.5 | 74.8        | 184    | 1     | 1VH0A2      |
| 25         | 710.5 | 74.0        | 184    | 1     | 1VH0A3      |
| 26         | 704.5 | 73.4        | 184    | 1     | 1VH0A1      |
| 27         | 690.5 | 71.9        | 167    | 2     | 025813      |
| 28         | 678.5 | 70.7        | 167    | 2     | 025843      |
| 29         | 665.5 | 69.3        | 162    | 2     | 025843      |

|    |       |      |     |   |        |
|----|-------|------|-----|---|--------|
| 30 | 660.5 | 68.7 | 169 | 2 | 025813 |
| 31 | 657.5 | 68.2 | 169 | 2 | 025813 |
| 32 | 656.5 | 68.2 | 169 | 2 | 025813 |
| 33 | 641.5 | 67.6 | 169 | 2 | 025813 |
| 34 | 630.5 | 67.5 | 169 | 2 | 025813 |
| 35 | 629.5 | 67.5 | 169 | 2 | 025813 |
| 36 | 628.5 | 67.5 | 169 | 2 | 025813 |
| 37 | 621.5 | 67.2 | 169 | 2 | 025813 |
| 38 | 620.5 | 67.2 | 169 | 2 | 025813 |
| 39 | 620.5 | 67.2 | 169 | 2 | 025813 |
| 40 | 622.5 | 67.2 | 169 | 2 | 025813 |
| 41 | 624.5 | 67.2 | 169 | 2 | 025813 |
| 42 | 621.5 | 67.2 | 169 | 2 | 025813 |
| 43 | 621.5 | 67.2 | 169 | 2 | 025813 |
| 44 | 621.5 | 67.2 | 169 | 2 | 025813 |
| 45 | 621.5 | 67.2 | 169 | 2 | 025813 |

## RESULTS

1VH0A2  
Interferon alpha 2 precursor (human) (M1150b v11)  
NCBI Reference Sequences (GenBank)  
Accession: AF044742  
Gene: IFNA2  
Protein: 188 amino acids  
Molecular Weight: 18.8 kDa  
Isoelectric Point: 4.5  
Function: Interferon alpha 2 precursor is a type I interferon. It is a single chain protein with a molecular weight of 18.8 kDa. It is secreted by virus-infected cells and by certain leukocytes. It has antiviral, antiproliferative, and immunomodulatory activities. It is the most abundant of the type I interferons. It is secreted by virus-infected cells and by certain leukocytes. It has antiviral, antiproliferative, and immunomodulatory activities. It is the most abundant of the type I interferons.























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RI Gene 10:1-10(1980).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8025454; PubMed 6157095;  
 RA Janiguchi T., Muntel N., Schwartzstein M., Nishida S., Muramatsu M.,  
 RA Weissmann C.;  
 RT "Human leukocyte and fibroblast interferons are structurally  
 RT related".  
 RL Nature 285:547-549(1980).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8114795; PubMed 6163083;  
 RA Goeddel D.V., Leung D.W., Dull T.F., Gross M., Jani P.M.,  
 RA McCandless F., Seeburg P.H., Gillich A., Vetterlin F., May E.W.;  
 RT "The structure of eight distinct cloned human leukocyte interferon  
 RT cDNAs".  
 RL Nature 290:20-26(1981).  
 RN (4)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8500392; PubMed 6479141;  
 RA Takeda K., Kioussis D., Weissmann C.;  
 RT "Two non-related human interferon-alpha genes with identical coding  
 RT regions".  
 RL PNAS 81:3186-3187(1984).  
 RN (5)  
 RP SEQUENCE OF 24-58.  
 RX MEDLINE=98087498; PubMed 9426112;  
 RA Nimmo T.A., Toole H., Park J., Kallish M.;  
 RT "Identification of nine interferon-alpha subtypes produced by Sendai  
 RT virus-induced human peripheral blood leukocytes".  
 RL Biochem. J. 329:295-302(1998).  
 RN (6)  
 RP POLYMERPHISM.  
 RX MEDLINE=20485144; PubMed 11032955;  
 RA Hussain M., Ni D., Gill D., Liao M.-L.;  
 RT "TNF-alpha-1a gene is the major variant in the North American  
 RT population".  
 RL J. Interferon Cytokine Res. 20:763-768(2000).  
 CC -1- FUNCTION: PROPOSED BY MACEPHEACRE: THE PRODUCTION OF TWO INTERFERON  
 CC ACTIVITIES: INTERFERON STIMULATES THE PRODUCTION OF TWO INTERFERON  
 CC A PROTEIN KINASE AND AN OLIGODEOXYRIBONUCLEOTIDE.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- POLYMERPHISM: Two forms exist: alpha-1a (shown here) and alpha-1b.  
 CC -1- MISCELLANEOUS: INTERFERONS ALPHA-1 AND ALPHA-1b HAVE IDENTICAL  
 CC PROTEIN SEQUENCES.  
 CC -1- SIMILARITY: PFC OPS TO THE INTERFERON ALPHA-1b AND ALPHA-1b.  
 CC FAMILY.  
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL copyright  
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 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed using by and for commercial  
 CC entities requires a license agreement (see http://www.ebi.ac.uk/submit/submit.html  
 CC or send an email to license@ebi.ac.uk).  
 CC -----  
 DR EMBL: J00210; AAB54403.1; -;  
 DR EMBL: J00537; CAA23798.1; -;  
 DR EMBL: J00538; CAA23799.1; -;  
 DR EMBL: X00803; CAA25381.1; -;  
 DR PIR: A01826; IYH01.  
 DR PIR: C23285; C23285.  
 DR HSSP: P01563; 2HIF.  
 DR GENE: HGNC:5417; IFNA1.  
 DR GENE: HGNC:5419; IFNA13.  
 DR MIM: 147660; -;  
 DR MIM: 147578; -;  
 DR InterPro: IPR000471; Interferon\_abd.  
 DR Pfam: PF00143; Interferon\_1.  
 DR PRINTS: PR00266; INTERFERONAR.  
 DR PRODOM: PD000550; Interferon\_abd; 1.  
 DR SMART: SM00076; Iabd; 1.  
 DR PROSITE: PS00252; INTERFERN\_A\_B; 1.

EMBL: J00210; AAB54403.1; -;  
 EMBL: J00537; CAA23798.1; -;  
 EMBL: J00538; CAA23799.1; -;  
 EMBL: X00803; CAA25381.1; -;  
 PIR: A01826; IYH01.  
 PIR: C23285; C23285.  
 HSSP: P01563; 2HIF.  
 GENE: HGNC:5417; IFNA1.  
 GENE: HGNC:5419; IFNA13.  
 MIM: 147660; -;  
 MIM: 147578; -;  
 InterPro: IPR000471; Interferon\_abd.  
 Pfam: PF00143; Interferon\_1.  
 PRINTS: PR00266; INTERFERONAR.  
 PRODOM: PD000550; Interferon\_abd; 1.  
 SMART: SM00076; Iabd; 1.  
 PROSITE: PS00252; INTERFERN\_A\_B; 1.  
 EMBL: J00210; AAB54403.1; -;  
 EMBL: J00537; CAA23798.1; -;  
 EMBL: J00538; CAA23799.1; -;  
 EMBL: X00803; CAA25381.1; -;  
 PIR: A01826; IYH01.  
 PIR: C23285; C23285.  
 HSSP: P01563; 2HIF.  
 GENE: HGNC:5417; IFNA1.  
 GENE: HGNC:5419; IFNA13.  
 MIM: 147660; -;  
 MIM: 147578; -;  
 InterPro: IPR000471; Interferon\_abd.  
 Pfam: PF00143; Interferon\_1.  
 PRINTS: PR00266; INTERFERONAR.  
 PRODOM: PD000550; Interferon\_abd; 1.  
 SMART: SM00076; Iabd; 1.  
 PROSITE: PS00252; INTERFERN\_A\_B; 1.













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Database version 9.1.4  
Copyright (c) 1994 - 2003 Compaq Inc.

OM protein - protein search, using sw model

Run on: January 17, 2003, 06:11:19 : Search time 55.004 seconds

(without alignment's)  
699,271 Million operations/sec

Title: us-09-915-873-4

Perfect score: 960

Sequence: 1 MAL1FALVALVALVLC\*KGSD\*.....RHHSTGSLMILKLRKQ1193

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 26602715 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP phyc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP yeast:\*  
14: SP unclassified:\*  
15: SP zfin:\*  
16: SP bacteria:\*  
17: SP archaea:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being plotted, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Match | Length | EB | ID      | Description      |
|------------|-------|-------|--------|----|---------|------------------|
| 1          | 814.5 | 84.8  | 189    | 6  | 095478  | 095478 satulins  |
| 2          | 789.5 | 82.2  | 189    | 6  | 095477  | 095477 satulins  |
| 3          | 776.5 | 80.9  | 189    | 4  | 014605  | 014605 home sapi |
| 4          | 756.5 | 78.8  | 189    | 4  | 014618  | 014618 home sapi |
| 5          | 739.5 | 77.0  | 181    | 4  | 014608  | 014608 home sapi |
| 6          | 688.5 | 71.7  | 166    | 4  | 090003  | 090003 home sapi |
| 7          | 677.5 | 70.6  | 166    | 4  | 090003  | 090003 home sapi |
| 8          | 596   | 62.1  | 190    | 11 | 090822  | 090822 murina    |
| 9          | 590   | 61.5  | 190    | 11 | 090835  | 090835 murina    |
| 10         | 584   | 60.7  | 201    | 11 | 090839  | 090839 murina    |
| 11         | 580.5 | 60.5  | 190    | 11 | 061718  | 061718 mus muscu |
| 12         | 573   | 59.7  | 190    | 11 | 0908504 | 0908504 murina   |
| 13         | 568   | 59.2  | 190    | 11 | 0908504 | 0908504 murina   |
| 14         | 567   | 59.2  | 197    | 11 | 0908507 | 0908507 murina   |
| 15         | 567   | 59.1  | 190    | 11 | 0908503 | 0908503 murina   |
| 16         | 565   | 58.9  | 180    | 11 | 0908506 | 0908506 murina   |

| Prod. No. | Score | Match | Length | EB | ID      | Description      |
|-----------|-------|-------|--------|----|---------|------------------|
| 17        | 564   | 58.7  | 189    | 6  | 095478  | 095478 satulins  |
| 18        | 564   | 58.7  | 189    | 6  | 095477  | 095477 satulins  |
| 19        | 564   | 58.7  | 189    | 4  | 014605  | 014605 home sapi |
| 20        | 564   | 58.7  | 189    | 4  | 014618  | 014618 home sapi |
| 21        | 564   | 58.7  | 181    | 4  | 014608  | 014608 home sapi |
| 22        | 564   | 58.7  | 166    | 4  | 090003  | 090003 home sapi |
| 23        | 564   | 58.7  | 166    | 4  | 090003  | 090003 home sapi |
| 24        | 564   | 58.7  | 190    | 11 | 090822  | 090822 murina    |
| 25        | 564   | 58.7  | 190    | 11 | 090835  | 090835 murina    |
| 26        | 564   | 58.7  | 201    | 11 | 090839  | 090839 murina    |
| 27        | 564   | 58.7  | 190    | 11 | 061718  | 061718 mus muscu |
| 28        | 564   | 58.7  | 190    | 11 | 0908504 | 0908504 murina   |
| 29        | 564   | 58.7  | 190    | 11 | 0908504 | 0908504 murina   |
| 30        | 564   | 58.7  | 197    | 11 | 0908507 | 0908507 murina   |
| 31        | 564   | 58.7  | 190    | 11 | 0908503 | 0908503 murina   |
| 32        | 564   | 58.7  | 180    | 11 | 0908506 | 0908506 murina   |
| 33        | 564   | 58.7  | 189    | 6  | 095478  | 095478 satulins  |
| 34        | 564   | 58.7  | 189    | 6  | 095477  | 095477 satulins  |
| 35        | 564   | 58.7  | 189    | 4  | 014605  | 014605 home sapi |
| 36        | 564   | 58.7  | 189    | 4  | 014618  | 014618 home sapi |
| 37        | 564   | 58.7  | 181    | 4  | 014608  | 014608 home sapi |
| 38        | 564   | 58.7  | 166    | 4  | 090003  | 090003 home sapi |
| 39        | 564   | 58.7  | 166    | 4  | 090003  | 090003 home sapi |
| 40        | 564   | 58.7  | 190    | 11 | 090822  | 090822 murina    |
| 41        | 564   | 58.7  | 190    | 11 | 090835  | 090835 murina    |
| 42        | 564   | 58.7  | 201    | 11 | 090839  | 090839 murina    |
| 43        | 564   | 58.7  | 190    | 11 | 061718  | 061718 mus muscu |
| 44        | 564   | 58.7  | 190    | 11 | 0908504 | 0908504 murina   |
| 45        | 564   | 58.7  | 190    | 11 | 0908504 | 0908504 murina   |

## RESULTS

## RESULT 1

095478

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1 CLASSIFICATION 424
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Odion, No. 5780921mg F.
4 REGISTRATION NUMBER: 24,618
5 REFERENCE/DOCKET NUMBER: 1125-006-0
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: (703) 413-3000
8 TELEFAX: (703) 413-2220
9
10 INDEX: 248556 opat hp
11
12 INFORMATION FOR SEQ ID NO: 4.
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 189 amino acids
15 TYPE: amino acid
16 TOPOLOGY: unknown
17 MOLECULE TYPE: protein
18 FEATURE:
19 NAME/KEY: Protein
20 LOCATION: 24..189
21 OTHER INFORMATION:
22
23 US-08-026-758-4 /note="11N-1.ppt"

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APPLICANT: KASTELI, IVOA

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TITLE OF INVENTION: NOVEL POLYMER-ALLEN AND 1,4-DITHIOLANES AND 1,4-DITHIOLANES

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US-09-915-873-4

Sequence: 30, Application US/099908193

Publication No. US2002019274A1

GENERAL INFORMATION:

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APPLICANT: MAIVANKAR, DRIEL M.

APPLICANT: PAJICARU, MARIANNA

TITLE OF INVENTION: NOVEL POLYMER-ALLEN AND 1,4-DITHIOLANES AND 1,4-DITHIOLANES

FILE REFERENCE: 21402-062

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CC selected cells. The complex comprises the gene encoding interferon  
CC releasably linked to a conjugate of nucleic acid binding agent and a  
CC ligand which binds to a component on the surface of the cell. The method  
CC is used for targeted expression of recombinant IFN in selected cells. In  
CC vivo or in vitro, particularly for treatment of hepatitis, several forms  
CC of cancer and leukemia and condyloma acuminatum, or for production of  
CC IFN for subsequent administration as exogenous protein.

SD Sequence 165 AA:

Query Match 100.0%; Score 851; PB 16; Length 165;  
Best local similarity 100.0%; Pred. No. 5,90-81;  
Matches 165; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CTPGCTHGTGSPPTLMLTACMPPTLHSCIKDRDPPTPEPEENCTGACATTVYHED 60  
DB 1 CTPGCTHGTGSPPTLMLTACMPPTLHSCIKDRDPPTPEPEENCTGACATTVYHED 60  
QY 61 GQHPHSTKSSAAMPPTTTPKPTVYQNMHDFVYGVVYVYPTTHKQVSTLAV 120  
DB 61 GQHPHSTKSSAAMPPTTTPKPTVYQNMHDFVYGVVYVYPTTHKQVSTLAV 120  
QY 121 KYEPPTLYIKKKRYKSPCAWVVAHIMSPSTNINQPSNKRK 175  
DB 121 KYEPPTLYIKKKRYKSPCAWVVAHIMSPSTNINQPSNKRK 175

RESULT 4  
AAW14015  
ID AAW14015 standard; Protein: 165 AA.  
AC AAW14015;  
XX 27-MAY-1997 (first entry)  
DE Interferon-alpha-2b.  
XX  
XX Interferon alpha-2b; recombinant; human; crystalline; metal; IFN alpha-  
KW controlled release system, IFNalpha2b.  
XX  
XX Homo sapiens.  
XX  
XX 085602242-A.  
XX  
XX 11-FEB-1997.  
XX  
XX 25-FEB-1993; 9308-0024320.  
XX  
XX 14-DEC-1994; 9408-0356021.  
XX  
XX 25-FEB-1993; 9308-0024320.  
XX  
XX (SCHE) SCHEKING CORP.  
XX  
XX Bruza A, Menemay C, Narahashan N, Narahashan H,  
XX Reichert P, Tindall S.  
XX  
XX WPI: 1997-141840/12.  
XX  
XX Produ. of crystalline metal interferon alpha-2 - 11.06 Interferon A and  
XX metal acetate  
XX  
XX Dislosure: Column 14-14; 14pp; English.

This sequence represents the recombinant human interferon alpha-2  
(IFNalpha2b). A crystalline metal version of this sequence is produced  
by the method of the invention. The method of the invention comprises  
forming an aqueous solution of IFNalpha2b and a metal acetate salt (copper  
zinc or cobalt acetate) at a pH of from 5 to 7, where the solution has  
an initial concentration of from 5-80 mg/ml IFNalpha2b and 70-120 mg/ml metal  
acetate salt. The solution is then warmed from an initial temperature of  
about 4 degrees C to 22 degrees C, until supersaturation occurs and metal  
IFNalpha2b crystals appear. The method is used to produce crystalline  
IFNalpha2b which is pharmaceutically useful in controlled release.

CC IFNalpha2b has been found to be useful in the treatment of hepatitis  
CC and has been found to be useful in the treatment of hepatitis  
XX Sequence 165 AA:  
CC  
CC Query Match 100.0%; Score 851; PB 16; Length 165;  
CC Best local similarity 100.0%; Pred. No. 5,90-81;  
CC Matches 165; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CTPGCTHGTGSPPTLMLTACMPPTLHSCIKDRDPPTPEPEENCTGACATTVYHED 60  
DB 1 CTPGCTHGTGSPPTLMLTACMPPTLHSCIKDRDPPTPEPEENCTGACATTVYHED 60  
QY 61 GQHPHSTKSSAAMPPTTTPKPTVYQNMHDFVYGVVYVYPTTHKQVSTLAV 120  
DB 61 GQHPHSTKSSAAMPPTTTPKPTVYQNMHDFVYGVVYVYPTTHKQVSTLAV 120  
QY 121 KYEPPTLYIKKKRYKSPCAWVVAHIMSPSTNINQPSNKRK 175  
DB 121 KYEPPTLYIKKKRYKSPCAWVVAHIMSPSTNINQPSNKRK 175

RESULT 4  
AAW14015  
ID AAW14015 standard; Protein: 165 AA.  
AC AAW14015;  
XX 27-MAY-1997 (first entry)  
DE Interferon-alpha-2b.  
XX  
XX Interferon alpha-2b; recombinant; human; crystalline; metal; IFN alpha-  
KW controlled release system, IFNalpha2b.  
XX  
XX Homo sapiens.  
XX  
XX 085602242-A.  
XX  
XX 11-FEB-1997.  
XX  
XX 25-FEB-1993; 9308-0024320.  
XX  
XX 14-DEC-1994; 9408-0356021.  
XX  
XX 25-FEB-1993; 9308-0024320.  
XX  
XX (SCHE) SCHEKING CORP.  
XX  
XX Bruza A, Menemay C, Narahashan N, Narahashan H,  
XX Reichert P, Tindall S.  
XX  
XX WPI: 1997-141840/12.  
XX  
XX Produ. of crystalline metal interferon alpha-2 - 11.06 Interferon A and  
XX metal acetate  
XX  
XX Dislosure: Column 14-14; 14pp; English.

This sequence represents the recombinant human interferon alpha-2  
(IFNalpha2b). A crystalline metal version of this sequence is produced  
by the method of the invention. The method of the invention comprises  
forming an aqueous solution of IFNalpha2b and a metal acetate salt (copper  
zinc or cobalt acetate) at a pH of from 5 to 7, where the solution has  
an initial concentration of from 5-80 mg/ml IFNalpha2b and 70-120 mg/ml metal  
acetate salt. The solution is then warmed from an initial temperature of  
about 4 degrees C to 22 degrees C, until supersaturation occurs and metal  
IFNalpha2b crystals appear. The method is used to produce crystalline  
IFNalpha2b which is pharmaceutically useful in controlled release.

















Search version 5.1.4  
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OM protein - protein search, using sw model

Run on: January 17, 2003, 06:50:48 ; Search time: 22.9 sec (without alignments)

692,560 Matches with updates/sec

Title: US-09-915-873-5

Perfect score: 851

Sequence: 1 COLICSHS2SPRFL162.....LHSSSPFLH2G22SPK 165

Scoring table: BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 28324 seqs, 9513122 residues

Total number of hits satisfying chosen parameters: 26/221

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 93

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR73:\*

2: PIR1:\*

3: PIR2:\*

4: PIR3:\*

5: PIR4:\*

6: PIR5:\*

7: PIR6:\*

8: PIR7:\*

9: PIR8:\*

10: PIR9:\*

11: PIR10:\*

12: PIR11:\*

13: PIR12:\*

14: PIR13:\*

15: PIR14:\*

16: PIR15:\*

17: PIR16:\*

18: PIR17:\*

19: PIR18:\*

20: PIR19:\*

Prod No is the number of results produced by a query. The total score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 851   | 100.0       | 165    | 2     | 178570      |
| 2          | 848   | 99.6        | 188    | 1     | 1VH0A2      |
| 3          | 728.5 | 85.6        | 189    | 1     | 1VH0A7      |
| 4          | 721.5 | 84.8        | 189    | 1     | 1VH016      |
| 5          | 719.5 | 84.5        | 189    | 2     | 125243      |
| 6          | 705.5 | 82.9        | 189    | 2     | 152347      |
| 7          | 703.5 | 82.7        | 189    | 2     | 151370      |
| 8          | 701.5 | 82.4        | 189    | 1     | 1VH014      |
| 9          | 695.5 | 81.7        | 176    | 2     | 156314      |
| 10         | 694.5 | 81.6        | 189    | 1     | 1VH048      |
| 11         | 692.5 | 81.4        | 181    | 2     | 156413      |
| 12         | 692.5 | 81.4        | 189    | 2     | 184464      |
| 13         | 691.5 | 81.3        | 189    | 1     | 1VH016      |
| 14         | 690.5 | 81.1        | 167    | 2     | 125843      |
| 15         | 690.5 | 81.1        | 189    | 1     | 1VH016      |
| 16         | 690.5 | 81.1        | 189    | 1     | 1VH045      |
| 17         | 688.5 | 80.9        | 189    | 1     | 1VH0A1      |
| 18         | 685.5 | 80.6        | 189    | 2     | 137584      |
| 19         | 684.5 | 80.4        | 189    | 1     | 1VH0A9      |
| 20         | 684.5 | 80.4        | 189    | 1     | 1VH018      |
| 21         | 678.5 | 79.7        | 167    | 2     | 125843      |
| 22         | 678.5 | 79.7        | 189    | 1     | 1VH0A0      |
| 23         | 678.5 | 79.7        | 189    | 2     | 153102      |
| 24         | 675.5 | 78.2        | 162    | 2     | 125843      |
| 25         | 674.5 | 78.1        | 189    | 1     | 1VH0A4      |
| 26         | 673.5 | 74.9        | 184    | 1     | 1VH0A4      |
| 27         | 673.5 | 74.4        | 184    | 1     | 1VH0A2      |
| 28         | 672.5 | 74.3        | 184    | 1     | 1VH0A3      |
| 29         | 672.5 | 74.3        | 184    | 1     | 1VH0A1      |

|    |       |       |     |   |        |
|----|-------|-------|-----|---|--------|
| 1  | 851   | 100.0 | 165 | 2 | 178570 |
| 2  | 848   | 99.6  | 188 | 1 | 1VH0A2 |
| 3  | 728.5 | 85.6  | 189 | 1 | 1VH0A7 |
| 4  | 721.5 | 84.8  | 189 | 1 | 1VH016 |
| 5  | 719.5 | 84.5  | 189 | 2 | 125243 |
| 6  | 705.5 | 82.9  | 189 | 2 | 152347 |
| 7  | 703.5 | 82.7  | 189 | 2 | 151370 |
| 8  | 701.5 | 82.4  | 189 | 1 | 1VH014 |
| 9  | 695.5 | 81.7  | 176 | 2 | 156314 |
| 10 | 694.5 | 81.6  | 189 | 1 | 1VH048 |
| 11 | 692.5 | 81.4  | 181 | 2 | 156413 |
| 12 | 692.5 | 81.4  | 189 | 2 | 184464 |
| 13 | 691.5 | 81.3  | 189 | 1 | 1VH016 |
| 14 | 690.5 | 81.1  | 167 | 2 | 125843 |
| 15 | 690.5 | 81.1  | 189 | 1 | 1VH016 |
| 16 | 690.5 | 81.1  | 189 | 1 | 1VH045 |
| 17 | 688.5 | 80.9  | 189 | 1 | 1VH0A1 |
| 18 | 685.5 | 80.6  | 189 | 2 | 137584 |
| 19 | 684.5 | 80.4  | 189 | 1 | 1VH0A9 |
| 20 | 684.5 | 80.4  | 189 | 1 | 1VH018 |
| 21 | 678.5 | 79.7  | 167 | 2 | 125843 |
| 22 | 678.5 | 79.7  | 189 | 1 | 1VH0A0 |
| 23 | 678.5 | 79.7  | 189 | 2 | 153102 |
| 24 | 675.5 | 78.2  | 162 | 2 | 125843 |
| 25 | 674.5 | 78.1  | 189 | 1 | 1VH0A4 |
| 26 | 673.5 | 74.9  | 184 | 1 | 1VH0A4 |
| 27 | 673.5 | 74.4  | 184 | 1 | 1VH0A2 |
| 28 | 672.5 | 74.3  | 184 | 1 | 1VH0A3 |
| 29 | 672.5 | 74.3  | 184 | 1 | 1VH0A1 |

692,560 Matches

## RESULTS

1: PIR73:\*

2: PIR1:\*

3: PIR2:\*

4: PIR3:\*

5: PIR4:\*

6: PIR5:\*

7: PIR6:\*

8: PIR7:\*

9: PIR8:\*

10: PIR9:\*

11: PIR10:\*

12: PIR11:\*

13: PIR12:\*

14: PIR13:\*

15: PIR14:\*

16: PIR15:\*

17: PIR16:\*

18: PIR17:\*

19: PIR18:\*

20: PIR19:\*

21: PIR20:\*

22: PIR21:\*

23: PIR22:\*

24: PIR23:\*

25: PIR24:\*

26: PIR25:\*

27: PIR26:\*

Query Match: 100.0

Query Length: 165

Query Start: 1

Query End: 165

Query Score: 851

Query E-value: 1e-165

Query Identity: 100.0

Query Coverage: 100.0

Query Alignment: 165/165

Query Gaps: 0

Query Mismatches: 0

Query Indels: 0

Query Ambiguities: 0

Query Repeats: 0

Query Truncations: 0

Query Other: 0

Query Total: 0

Query Status: 0

Query Errors: 0

Query Warnings: 0

Query Match: 100.0

Query Length: 165

Query Start: 1

Query End: 165

Query Score: 851

Query E-value: 1e-165

Query Identity: 100.0

Query Coverage: 100.0

Query Alignment: 165/165

Query Gaps: 0

Query Mismatches: 0

Query Indels: 0

Query Ambiguities: 0

Query Repeats: 0

Query Truncations: 0

Query Other: 0

Query Total: 0

Query Status: 0

Query Errors: 0

Query Warnings: 0









Interferon alpha-14b precursor - human

NCBI accession: M16N-alpha14b Type 1 Interferon

C-species: Homo sapiens (man)

C-date: 29-Nov-1997 #sequence accession: 29 Nov 1997 #status: human 16 Feb 1999

C-accession: E23753

J. Mol. Biol. 185, 227-260, 1995

A: title: Structural relationship of human Interferon alpha genes and pseudogenes.

A: reference number: A92916; MIM:6037205; PMID:857246

A: accession: E23753

A: molecule type: DNA

A: residues: 1-189 <HEX>

A: cross-references: CP: X02655; MIM: 603720; PMID: 857246

A: gene: GPR-1FN1

A: cross-references: GDB: 119126; MIM: 147660

A: map position: 9p22-9p23

C: superfamily: Interferon alpha

C: keywords: antiviral

F1-23/Domain: signal sequence #status: predicted - S17

F24-189/Product: Interferon alpha-14b #status: predicted - M1

F1-4-152/52-152/Signal: 1081 #status: predicted

Query Match

Best Local Similarity

Matches

136

Conservative

12

Mismatches

179

Gap

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Interferon alpha-14b precursor - human

NCBI accession: M16N-alpha14b Type 1 Interferon

C-species: Homo sapiens (man)

C-date: 29-Nov-1997 #sequence accession: 29 Nov 1997 #status: human 16 Feb 1999

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C: keywords: antiviral

F1-23/Domain: signal sequence #status: predicted - S17

F24-189/Product: Interferon alpha-14b #status: predicted - M1

F1-4-152/52-152/Signal: 1081 #status: predicted

Query Match

Best Local Similarity

Matches

136

Conservative

12

Mismatches

179

Gap

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Interferon alpha-14b precursor - human

NCBI accession: M16N-alpha14b Type 1 Interferon

C-species: Homo sapiens (man)

C-date: 29-Nov-1997 #sequence accession: 29 Nov 1997 #status: human 16 Feb 1999

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F24-189/Product: Interferon alpha-14b #status: predicted - M1

F1-4-152/52-152/Signal: 1081 #status: predicted

Query Match

Best Local Similarity

Matches

136

Conservative

12

Mismatches

179

Gap

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Interferon alpha-14b precursor - human

NCBI accession: M16N-alpha14b Type 1 Interferon

C-species: Homo sapiens (man)

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C-accession: E23753

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Query Match

Best Local Similarity

Matches

136

Conservative

12

Mismatches

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F24-189/Product: Interferon alpha-14b #status: predicted - M1

F1-4-152/52-152/Signal: 1081 #status: predicted

Query Match

Best Local Similarity

Matches

136

Conservative

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Mismatches

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Gap

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Interferon alpha-14b precursor - human

NCBI accession: M16N-alpha14b Type 1 Interferon

C-species: Homo sapiens (man)

C-date: 29-Nov-1997 #sequence accession: 29 Nov 1997 #status: human 16 Feb 1999

C-accession: E23753

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C: keywords: antiviral

F1-23/Domain: signal sequence #status: predicted - S17

F24-189/Product: Interferon alpha-14b #status: predicted - M1

F1-4-152/52-152/Signal: 1081 #status: predicted

Query Match

Best Local Similarity

Matches

136

Conservative

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Mismatches

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Gap

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Comptore version 5.1.3  
Copyright (c) 1993 - 2003 Comptore Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 05:28:45 ; Search time: 11.6446 seconds

(without alignment)

Title: us-09-915-873-5

Perfect score: 851

Sequence: 1 CDLP0THUSKRLIMLAW.....LIMPHSLINLISPKR...L

Scoring table: BLASTP62

Capot 10.0 ; Gapext 0.5

Searched: 112992 seqs, 1176426 residues

Total number of hits satisfying chosen parameters: 112792

Minimum PB seq length: 0

Maximum PB seq length: 200000000

Post-processing: Minimum Match 0.8

Maximum Match 100%

Listing first 45 summaries

Database: SWISSPROT\_1993\*

Pred. No. is the number of results predicted by number to be used

Score greater than or equal to the score of the result being predicted

and is derived by analysis of the total score distribution

Result No. Score Match Length PB ID

8

SUMMARIES

1 848 99.6 199 1 INA2\_HUMAN

2 728.5 85.6 189 1 INA2\_HUMAN

3 721.5 84.8 189 1 INA2\_HUMAN

4 701.5 82.4 189 1 INA2\_HUMAN

5 694.5 81.6 189 1 INA2\_HUMAN

6 694.5 81.6 189 1 INA2\_HUMAN

7 692.5 81.6 189 1 INA2\_HUMAN

8 691.5 81.3 189 1 INA2\_HUMAN

9 690.5 81.1 189 1 INA2\_HUMAN

10 688.5 80.9 189 1 INA2\_HUMAN

11 684.5 80.4 189 1 INA2\_HUMAN

12 679.5 79.7 189 1 INA2\_HUMAN

13 673.5 74.9 184 1 INA2\_HUMAN

14 633.5 74.4 184 1 INA2\_HUMAN

15 632.5 74.3 184 1 INA2\_HUMAN

16 632.5 74.3 184 1 INA2\_HUMAN

17 577.5 67.9 189 1 INA2\_HUMAN

18 562.5 66.1 189 1 INA2\_HUMAN

1 562.5 66.1 189 1 INA2\_HUMAN  
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# RESULTS

## INA2\_HUMAN

### STANDARD

#### 1

##### INA2\_HUMAN

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RT Identification of heme interferon-alpha subtypes produced by Sema-1  
 RT Virus-induced human peripheral blood monocytes.  
 RN Biochem. J. 329:295-302(1998).  
 RN [4].  
 RP POLYMERPHISM.  
 RP MEDLINE:97474112, PubMed 9145434;  
 RA Hussain M., Gill D.S., Liao M.-L.;  
 RT "Both variant forms of Interferon-alpha4 gene (IFNA4 and IFNA4) are  
 RT present in the human population."  
 RL J. Interferon Cytokine Res. 17:559-566(1997).  
 CC -1- FUNCTION: PROTECT BY NUCLEOTIDES, PROTECT BY NUCLEOTIDES.  
 CC ACTIVITIES: INTERFERON STIMULATES THE PRODUCTION OF TWO INTERFERON  
 CC A PROTEIN KINASE AND AN ULTRAVIOLET SENSITIVE.  
 CC -1- STRUCTURAL LOCATION: Secreted.  
 CC -1- POLYMORPHISM: Two forms exist: alpha-4a and alpha-4b (shown here).  
 CC They seem to be equally abundant.  
 CC -1- SIMILARITY: Belongs to the INTERFERON ALPHA, BETA AND GAMMA  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X02955, CAA26701.1;  
 DR EMBL: M27318, AAA2726.1;  
 DR PIR: E27531, IMH04b,  
 DR HSSP: P01563, ZHIE,  
 DR Genew: HGNC:5425, IFNA4,  
 DR MIM: 147564;  
 DR InterPro: IP000471, Interferon\_alph.  
 DR Pfam: PF00143, Interferon\_1.  
 DR PRINTS: PR00266, INTERFERONAB,  
 DR PRODOM: PD000550, Interferon\_alph. 1,  
 DR SMART: SM00076, IFab0.1,  
 DR PROSITE: PS00252, INTERFERON\_A\_P1.1,  
 DR Cytokine: Antiviral; Multigene family; Polymorphism: Simul.  
 FT STNAL 1 23  
 FT CLAIN 24 189 INTERFERON ALPHA 4  
 FT DISULFID 24 122 BY SIMILARITY.  
 FT DISULFID 52 162 BY SIMILARITY.  
 FT VARIANT 74 74 I - A (IN ALPHA-4A).  
 FT /FIELD VAR:01002.  
 FT VARIANT 137 137 V - E (IN ALPHA-4A).  
 FT /FIELD VAR:01300.  
 SD SEQUENCE 189 AA, 21962 MD, 41567 SY, 28771, 28771.  
 Query Match 81.6%; Score 594.5; DR 1; Length 189;  
 Host Local Similarity 81.6%; Prod. No. 5, 80-57;  
 Matches 136; Conservative 12; Mismatches 17; Incons 1; Gap 1;  
 QY 1 TELQTHSTGSRPTMIAAGNAPSTSTKPKDQVSTPDR INKAFVSTPDR  
 DB 24 QHAPQTHSTGSRPTMIAAGNAPSTSTKPKDQVSTPDR INKAFVSTPDR  
 QY 1 TELQTHSTGSRPTMIAAGNAPSTSTKPKDQVSTPDR INKAFVSTPDR  
 DB 84 QHAPQTHSTGSRPTMIAAGNAPSTSTKPKDQVSTPDR INKAFVSTPDR  
 QY 1 TELQTHSTGSRPTMIAAGNAPSTSTKPKDQVSTPDR INKAFVSTPDR  
 DB 144 QHAPQTHSTGSRPTMIAAGNAPSTSTKPKDQVSTPDR INKAFVSTPDR  
 RESULT 6  
 INAC\_HUMAN STANDARD; PIR: 189 AA.  
 AC P01571: Q14649;  
 DT 21-JUL-1986 (Ref. 01, Created)  
 DT 01-OCT-1994 (Ref. 30, Last sequence update)

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 QY 1 TELQTHSTGSRPTMIAAGNAPSTSTKPKDQVSTPDR INKAFVSTPDR  
 DB 144 QHAPQTHSTGSRPTMIAAGNAPSTSTKPKDQVSTPDR INKAFVSTPDR  
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3 FILING DATE:  
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5 CLASSIFICATION: 800  
6  
7 ATTORNEY/AGENT INFORMATION:  
8 NAME: Stuart, Donald R  
9  
10 TELECOMMUNICATION INFORMATION:  
11  
12 TELEPHONE: 317 437 4816  
13  
14 TELEFAX: 317 337 4847  
15  
16 INFORMATION FOR SEQ ID NO. 1:  
17  
18 SEQUENCE CHARACTERISTICS:  
19  
20 LENGTH: 10160 base pairs  
21  
22 TYPE: nucleic acid  
23  
24 STRANDEDNESS: double  
25  
26 TOPOLOGY: circular  
27  
28 MOLECULE TYPE: DNA  
29  
30 HQ-09-007-319A-8

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| Best Local Similarity: | 100.0%       | Prod. No.  | 4.26       | 27          |
| Matches 118:           | Conservative | 0:         | Mismatches | 0:          |
|                        |              |            | Indels     | 0:          |
|                        |              |            | Gaps       | 0:          |

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DQ 496 TGCATCTGATGATTACCTTCACTAAGCCAAAGTTTCCTGGAGCAGCGAGGTCTGCTCTG

DO 3085 TGCATCTGATGATTACCTTGAATAAGCAAAGCTTTCTGGAGCAGCGAGGTCTGCTCTG

RESULT 12  
US-09-097-419A-4  
Sequence '9, Application US/09/073108  
Inventor: N. J. ...

GENERAL INFORMATION:  
 APPLICANT: Ainsley, Michael  
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 TITLE OF INVENTION: Regulatory Sequences for Immunologic Interactions  
 NUMBER OF SEQUENCES: 59

ADDRESS: Dowling Patent Impairment  
STREET: 9340 Zionsville Road  
CITY: Indianapolis  
STATE: Indiana  
COUNTRY: USA  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/0037, 319A  
FILING DATE:

1 TELECOMMUNICATIONS INFORMATION  
 2 NAME: Stuart, Donald R  
 3 TELECOMMUNICATIONS INFORMATION  
 4 TELEPHONE: 317 347 4816  
 5 TELEFAX: 317 347 4847  
 6 INFORMATION FOR SFO ID NO: 9  
 7 SEQUENCE CHARACTERISTICS:  
 8 LENGTH: 11784 base pairs  
 9 TYPE: nucleic acid  
 10 STRANDEDNESS: double

[illegible][illegible][illegible]

Received 10 October 1994  
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[illegible][illegible][illegible]

2004y, Muth, 2004z, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 2680, 2681, 2682, 2683, 268

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Fri Jan 17 09:14:20 2003

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